

BATCH

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/609,146

ENTERED

CRF Processing Date: 1/30/2001
Edited by: [Signature]
Verified by: [Signature] (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:

- ☒ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:

- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☒ Corrected an obvious error in the response, specifically:
corrected C1207 response
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

BATCH

RAW SEQUENCE LISTING DATE: 01/30/2001
 PATENT APPLICATION: US/09/609,146 TIME: 11:00:39

Input Set : A:\607941.app
 Output Set: N:\CRF3\01302001\I609146.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Bonini et al, James A.
 5 <120> TITLE OF INVENTION: DNA Encoding SNORF62 And SNORF72 Receptors
 7 <130> FILE REFERENCE: 60794-B
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/609,146
 C--> 10 <141> CURRENT FILING DATE: 2000-06-30
 12 <150> PRIOR APPLICATION NUMBER: 09/558,099
 13 <151> PRIOR FILING DATE: 2000-04-25
 15 <160> NUMBER OF SEQ ID NOS: 46
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1318
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
 27 <400> SEQUENCE: 1
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 29 ctctgtcctc cctggagacc tgtaccacag gggtgcaagg aaccccatgg ctgcaatagg 120
 30 cagtgcggcc agggggcact ttgaccctga ggacttgaac ctgactgacg aggcactgag 180
 31 actcaagtac ctggggccccc agcagacaga gctgttcatg cccatctgtg ccacatacct 240
 32 gctgatcttc gtgggtgggc ctgtgggcaa tgggctgacc tgtctggtca tctgcccga 300
 33 caaggccatg cgcacgccta ccaactacta cctcttcagc ctggccgtgt cggacctgct 360
 34 ggtgctgctg gtgggcctgc cctggagct ctatgagatg tggcacaact accccttct 420
 35 gctgggctgt ggtggtgct atttccgcac gctactgttt gagatggtct gccctggctc 480
 36 agtgctcaac gtcactgccc tgagcgtgga acgctatgtg gccgtggtgc acccaactca 540
 37 ggcaggttcc atggtgacgc gggcccatgt ggcgcgagtg ctggggccg tctggggtct 600
 38 tgccatgctc tgcctcctgc ccaacaccag cctgcacggc atccggcagc tgcacgtgcc 660
 39 ctgcccgggc ccagtgccag actcagctgt ttgcatgctg gtccgcccac gggccctcta 720
 40 caacatggta gtgcagacca ccgcgtgct ctctctctgc ctgcccatgg ccatcatgag 780
 41 cgtgctctac ctgctcattg ggctgcgact gcggcgggag aggetgctgc tcatgcagga 840
 42 ggccaagggc aggggctctg cagcagccag gtccagatac acctgcaggc tccagcagca 900
 43 cgatcggggc cggagacaag tgaccaagat gctgtttgtc ctggctgtgg tgtttggcat 960
 44 ctgctgggce ccgttccacg ccgaccgct catgtggagc gtcgtgtcac agtggacaga 1020
 45 tggcctgcac ctggccttcc agcacgtgca cgtcatctcc ggcatcttct tctacctggg 1080
 46 ctgcccggcc aacccctgct tctatagcct catgtccagc cgtctccgag agaccttcca 1140
 47 ggagggccctg tgccctgggg cctgtgcca tcgctcaga ccccgccaca gctcccacag 1200
 48 cctcagcagg atgaccacag gcagcaccct gtgtgatgtg ggctccctgg gcagctgggt 1260
 49 ccacccctct gctgggaacg atggcccaga ggcgcagcaa gagaccgatc catctga 1318
 52 <210> SEQ ID NO: 2
 53 <211> LENGTH: 426
 54 <212> TYPE: PRT
 55 <213> ORGANISM: Artificial Sequence
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
 60 <400> SEQUENCE: 2
 61 Met Thr Pro Leu Cys Leu Asn Cys Ser Val Leu Pro Gly Asp Leu Tyr
 62 1 5 10 15

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64 Pro Gly Gly Ala Arg Asn Pro Met Ala Cys Asn Gly Ser Ala Ala Arg
65           20           25           30
67 Gly His Phe Asp Pro Glu Asp Leu Asn Leu Thr Asp Glu Ala Leu Arg
68           35           40           45
70 Leu Lys Tyr Leu Gly Pro Gln Gln Thr Glu Leu Phe Met Pro Ile Cys
71           50           55           60
73 Ala Thr Tyr Leu Leu Ile Phe Val Val Gly Ala Val Gly Asn Gly Leu
74 65           70           75           80
76 Thr Cys Leu Val Ile Leu Arg His Lys Ala Met Arg Thr Pro Thr Asn
77           85           90           95
79 Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Val
80           100          105          110
82 Gly Leu Pro Leu Glu Leu Tyr Glu Met Trp His Asn Tyr Pro Phe Leu
83           115          120          125
85 Leu Gly Val Gly Gly Cys Tyr Phe Arg Thr Leu Leu Phe Glu Met Val
86           130          135          140
88 Cys Leu Ala Ser Val Leu Asn Val Thr Ala Leu Ser Val Glu Arg Tyr
89 145          150          155          160
91 Val Ala Val Val His Pro Leu Gln Ala Arg Ser Met Val Thr Arg Ala
92           165          170          175
94 His Val Arg Arg Val Leu Gly Ala Val Trp Gly Leu Ala Met Leu Cys
95           180          185          190
97 Ser Leu Pro Asn Thr Ser Leu His Gly Ile Arg Gln Leu His Val Pro
98           195          200          205
100 Cys Arg Gly Pro Val Pro Asp Ser Ala Val Cys Met Leu Val Arg Pro
101           210          215          220
103 Arg Ala Leu Tyr Asn Met Val Val Gln Thr Thr Ala Leu Leu Phe Phe
104 225          230          235          240
106 Cys Leu Pro Met Ala Ile Met Ser Val Leu Tyr Leu Leu Ile Gly Leu
107           245          250          255
109 Arg Leu Arg Arg Glu Arg Leu Leu Leu Met Gln Glu Ala Lys Gly Arg
110           260          265          270
112 Gly Ser Ala Ala Ala Arg Ser Arg Tyr Thr Cys Arg Leu Gln Gln His
113           275          280          285
115 Asp Arg Gly Arg Arg Gln Val Thr Lys Met Leu Phe Val Leu Val Val
116           290          295          300
118 Val Phe Gly Ile Cys Trp Ala Pro Phe His Ala Asp Arg Val Met Trp
119 305          310          315          320
121 Ser Val Val Ser Gln Trp Thr Asp Gly Leu His Leu Ala Phe Gln His
122           325          330          335
124 Val His Val Ile Ser Gly Ile Phe Phe Tyr Leu Gly Ser Ala Ala Asn
125           340          345          350
127 Pro Val Leu Tyr Ser Leu Met Ser Ser Arg Phe Arg Glu Thr Phe Gln
128           355          360          365
130 Glu Ala Leu Cys Leu Gly Ala Cys Cys His Arg Leu Arg Pro Arg His
131           370          375          380
133 Ser Ser His Ser Leu Ser Arg Met Thr Thr Gly Ser Thr Leu Cys Asp
134 385          390          395          400
136 Val Gly Ser Leu Gly Ser Trp Val His Pro Leu Ala Gly Asn Asp Gly

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137          405          410          415
139 Pro Glu Ala Gln Gln Glu Thr Asp Pro Ser
140          420          425
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 1298
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
151 <400> SEQUENCE: 3
152 aggggaggct caggcccttg attttaatgt cagggatgga aaaacttcag aatgcttcct 60
153 ggatctacca gcagaaacta gaaagatccat tccagaaaaca cctgaacagc accgaggagt 120
154 atctggcctt cctctgcgga cctcggcgca gccacttctt cctcccgctg tctgtggtgt 180
155 atgtgccaat ttttgggtg ggggtcattg gcaatgtcct ggtgtgcctg gtgattctgc 240
156 agcaccaggc tatgaagacg cccaccaact actacctctt cagcctggcg gtctctgacc 300
157 tcttggtcct gctccttgga atgccctgg aggtctatga gatgtgacgc aactaccctt 360
158 tcttgttcgg gccctggtgc tctacttca agacggccct ctttgagacc gtgtgcttcg 420
159 cctccatcct cagcatcacc accgtcagcg tggagcgcta cgtggccatc ctacaccctt 480
160 tccgcgccaa actgcagagc acccggcgcg gggccctcag gatcctcgcg atcgtctggg 540
161 gcttctccgt gctctctccc ctgcccaaca ccagcatcca tggcatcaag ttccactact 600
162 tccccaatgg gtccctggtc ccagggttcg ccacctgtac ggtcatcaag cccatgtgga 660
163 tctacaattt catcatccag gtcacctcct tctatttcta cctcctcccc atgaactgtc 720
164 tcagtgtcct ctactacctc atggcactca gactaaagaa agacaaatct cttgaggcag 780
165 atgaagggaa tgcaaatatt caaagacctc gcagaaaatc agtcaacaag atgctgtttg 840
166 tcttggtctt agtgtttgct atctgttggg ccccgttcca cattgaccga ctctcttcca 900
167 gcttgttgga ggagtggagt gaatccctgg ctgctgtgtt caacctcgtc catgtggtgt 960
168 caggtgtctt ctctacctg agctcagctg tcaaccccat tatctataac ctactgtctc 1020
169 gccgcttcca ggcagcattc cagaatgtga tctctctttt ccacaaacag tggcactccc 1080
170 agcatgacc cagattgcca cctgccacgc ggaacatctt cctgacagaa tgccactttg 1140
171 tggagctgac cgaagatata ggtccccaat tcccatgtca gtcctccatg cacaactctc 1200
172 acctcccaac agccctctct agtgaacaga tgtcaagaac aaactatcaa agcttccact 1260
173 ttaacaaaac ctgaattctt tcagagctga ctctcctc 1298
176 <210> SEQ ID NO: 4
177 <211> LENGTH: 415
178 <212> TYPE: PRT
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
184 <400> SEQUENCE: 4
185 Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln
186 1 5 10 15
188 Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
189 20 25 30
191 Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
192 35 40 45
194 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
195 50 55 60
197 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
198 65 70 75 80

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200 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
201      85      90      95
203 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
204      100      105      110
206 Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
207      115      120      125
209 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
210      130      135      140
212 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
213 145      150      155      160
215 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
216      165      170      175
218 Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
219      180      185      190
221 Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
222      195      200      205
224 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
225      210      215      220
227 Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
228 225      230      235      240
230 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
231      245      250      255
233 Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val
234      260      265      270
236 Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg
237      275      280      285
239 Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val
240      290      295      300
242 Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser
243 305      310      315      320
245 Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala
246      325      330      335
248 Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln
249      340      345      350
251 His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
252      355      360      365
254 Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
255      370      375      380
257 Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
258 385      390      395      400
260 Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
261      405      410      415
264 <210> SEQ ID NO: 5
265 <211> LENGTH: 25
266 <212> TYPE: PRT
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
272 <400> SEQUENCE: 5

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RAW SEQUENCE LISTING
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273 Phe Arg Val Asp Glu Glu Phe Gln Ser Pro Phe Ala Ser Gln Ser Arg
274   1           5           10           15
276 Gly Tyr Phe Leu Phe Arg Pro Arg Asn
277   20           25
280 <210> SEQ ID NO: 6
281 <211> LENGTH: 25
282 <212> TYPE: PRT
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
288 <400> SEQUENCE: 6
289 Phe Lys Val Asp Glu Glu Phe Gln Gly Pro Ile Val Ser Gln Asn Arg
290   1           5           10           15
292 Arg Tyr Phe Leu Phe Arg Pro Arg Asn
293   20           25
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 23
298 <212> TYPE: PRT
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
304 <400> SEQUENCE: 7
305 Tyr Lys Val Asn Glu Tyr Gln Gly Pro Val Ala Pro Ser Gly Gly Phe
306   1           5           10           15
308 Phe Leu Phe Arg Pro Arg Asn
309   20
312 <210> SEQ ID NO: 8
313 <211> LENGTH: 8
314 <212> TYPE: PRT
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
320 <400> SEQUENCE: 8
321 Tyr Phe Leu Phe Arg Pro Arg Asn
322   1           5
325 <210> SEQ ID NO: 9
326 <211> LENGTH: 24
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
333 <400> SEQUENCE: 9
334 ccacgaagat cagcaggtat gtgg                24
337 <210> SEQ ID NO: 10
338 <211> LENGTH: 24
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/609,146

DATE: 01/30/2001

TIME: 11:00:40

Input Set : A:\607941.app

Output Set: N:\CRF3\01302001\I609146.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date